

Re-run

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/787,016A

DATE: 05/08/2002

TIME: 10:47:46

Input Set : N:\paola\US09787016A.raw

Output Set: N:\CRF3\05082002\I787016A.raw

1 <110> APPLICANT: Alonso, Carlos  
 2 Domingo, David  
 3 Grandien, Alf  
 4 Leonardo, Esther  
 5 Martinez, Pedro  
 6 <120> TITLE OF INVENTION: Genes Encoding for the Human and Murine Death Inducer-  
 Obliterator-1  
 7 <130> FILE REFERENCE: 46309-253995  
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/787,016A  
 9 <141> CURRENT FILING DATE: 2001-06-18  
 10 <150> PRIOR APPLICATION NUMBER: PCT/GB99/03019  
 11 <151> PRIOR FILING DATE: 1999-09-10  
 12 <160> NUMBER OF SEQ ID NOS: 4  
 13 <170> SOFTWARE: PatentIn version 3.0  
 15 <210> SEQ ID NO: 1  
 16 <211> LENGTH: 2610  
 17 <212> TYPE: DNA  
 18 <213> ORGANISM: Homo sapiens  
 19 <400> SEQUENCE: 1

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22	cctgttactc	gtgaacagtg	gctgacaaca	gtgttggtgt	gagcctggct	gtctgcttgg	180
23	acccagaggt	ttcgtctgcc	agggtttttg	gttgatttta	ggatttcagg	gaaaagtgtc	240
24	caagctttca	gtgttgagc	aggtatggac	gacaaaggcg	acccgagcaa	tgaggaggca	300
25	cctaaggcca	tcaaaccac	cagcaaagag	ttcaggaaaa	catgggggtt	tcgaaggacc	360
26	actatcgcca	agcgagagg	cgcaggggac	gcggaggctg	accactgga	gccgccaccc	420
27	ccacagcagc	agctgggcct	gtccctgcgg	cgcagtggga	ggcagcccaa	gcgcactgag	480
28	cgcgtggagc	agttcctgac	cattgcgcgg	cgccgcggca	ggaggagcat	gcctgtctcc	540
29	ctggagggatt	ctggtgagcc	cacgtcctgc	cccgccacag	acgccgagac	agcctccgag	600
30	ggcagcgtgg	aaagcgcttc	tgagaccaga	agcggccccc	agtctgcttc	cacagctgtg	660
31	aaggaacgac	cagcctcttc	tgaaaagggtg	aaaggagggg	atgaccacga	tgacacctcc	720
32	gatatgtaca	gcgatggcct	gaccttgaaa	gagcttcaga	atcgccctcg	caggaagcgg	780
33	gaacaggagc	ccactgagag	gcccctgaaa	gggatccaga	gtcgctgcg	gaagaagcgc	840
34	cgggaggagg	gtcccgccga	gactgtgggc	tccgaggcca	gtgacactgt	ggagggcgtc	900
35	ctgcccagta	agcaggagcc	cgagaacgat	caggggggtg	tgtcccaggc	tgggaaagat	960
36	gacagagaga	gtaagttgga	gggaaaaggcg	gctcaggaca	tcaaagatga	ggagcctgga	1020
37	gacttggggc	gaccgaagcc	tgaatgtgag	ggttacgacc	ccaacgccct	gtattgcatt	1080
38	tgccgcgagc	ctcacaaaca	cagggtttatg	atttgctgtg	accgctgtga	agaatgggtt	1140
39	catggcgatt	gtgtgggcat	ttctgaggct	cgagggaggc	ttttggaaaag	gaatggggaa	1200
40	gactatatct	gccccaaactg	caccattctg	caagtgcagg	atgagactca	ttcagaaacg	1260
41	gcagatcagc	aggaagctaa	atggagacct	ggagatgctg	atggcaccga	ttgtacaagt	1320
42	ataggaacaa	tagagcagaa	gtctagcgaa	gaccaaggga	taaagggtag	aattgagaaa	1380
43	gctgcaaadc	caagtggcaa	gaagaaactc	aagatcttcc	agcctgtgat	agaggcgctc	1440
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46	aaagaacaga	agccaaagcc	taaagaaaag	atgaagatga	agccagagaa	gcccagtctt	1620
47	ccgaaatgcy	gtgctcaggc	aggtattaaa	atctcttctg	tgacaaagag	accagctcca	1680
48	gaaaaaaaag	agaccacagt	gaagaaggca	gtggtggtcc	ctgcgcggag	tgaagcactc	1740
49	gggaaggaa	cagcttgtag	gagcagcacg	ccgtcgtggg	cgagcgatca	caattacaat	1800
50	gcagtaaagc	cagaaaagac	tgctgctccc	tcgcccgtcac	tggtgtataa	atgtatgtat	1860
51	cacctagggy	ttggcctcct	ggacccctcc	cgttctttct	ggatagccat	cccctgggcc	1920
52	tgtccaggac	tggtgagttg	agctttgtgt	taagctgac	acagacaccg	gctgcacat	1980
53	cagcgggaag	cagagcccat	gtccaggatg	cctcctgctg	ccctgtgtcc	atccctagtc	2040
54	tgctcaggact	tcctgtcact	gttttccaaa	gctgtaaacc	tcactggtga	acgttcacct	2100
55	taatgattga	ttctttaatc	tctgttttca	ctctcaggct	ctggtaagta	tttgatttct	2160
56	cttcatccca	gtctgattgc	atagccacac	tgcccggcac	gccacatcca	cccctgtctg	2220
57	cacatgagtt	gttctgacaa	cagcgtgta	tacgtctcag	tttttccaca	ttgtccacgg	2280
58	ccagcacatg	aaagcatcac	ttctttttta	tggtgtggga	atctttgcaa	gttagtggtg	2340
59	catctgattt	tcaggtgtac	atcttttttt	gactgggcag	ataggggatt	tttttttttt	2400
60	tccatgtccg	attcacacgc	tacacacca	catgaacaca	ttcgaacttc	gaaggcacac	2460
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62	aggacgcgtg	ccttggaact	ggtattctac	atgtgactgg	ctttcttgcc	ctcgtctctt	2580
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73	tatgtaggat	ttccagccaa	aggtttccaa	gctttcagtt	ttgggacagg	tatggatgat	240
74	aaagggcacc	tgagcaatga	ggaagcacc	aaggctatca	aaccaccag	taaggagttc	300
75	aggaaaacct	gggtttttcg	aagaaccacg	attgccaaac	gtgagggtgc	aggagacacg	360
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81	gaggaagaag	acacctctga	cagttagcagt	gatggcctta	cggtgaagga	acttcagaac	720
82	cgcttccgga	gaaagcgaga	gcaagaacct	gtggagaggt	ccctgagagg	cagtcagaat	780
83	cgcttaggga	agaagcgag	agaggaagat	tctgccgaaa	ctgggaggtg	ccaaataggc	840
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85	tcccagtcag	agacagatga	catagaaaaa	cagttggaag	ggaaggcgac	tcagggaaat	960
86	acagaggaaa	accccgagg	agcgggcaaa	ccaaagcctg	agtgtgaggt	ttacgacccc	1020
87	aatgccctgt	actgcatctg	ccgccagcct	cacaacaaca	ggtttatgat	ctgctgtgat	1080
88	cgggtgtagg	agtgggtcca	tggtgactgt	tggggtatct	ctgaggcccg	aggcggtctc	1140
89	ctggaaaagg	acgggggaag	ctacatctgc	ccaaattgca	ccattttgca	agtgcaggat	1200
90	gagacaaacg	gtagcgccac	caatgagcag	gactctgggt	gcagatctgt	gggtgctgat	1260
91	ggcacagact	gcacaagcat	agggacagta	gagcagaagt	ccggagaaga	ccagggcata	1320
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93	cctgtcgtag	aggctcctgg	tgctcctaaa	tgcatgtggc	ctgggtgttc	cagtgtagca	1440
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TIME: 10:47:46

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101     ctgggtggct gcctggggct gtctaggacc agagtccttg gtgttctggt gctgatagta 1920
102     gccagcagct cactgccagc cagaagcaga taccaagatg cctctggacc ccaggtgttc 1980
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108     caatttgtgt ctatttcaca tactacacac ctacataaac aggtttgaat tttgaaggtc 2340
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116     ggggtgtgaac tcagagtgtt ggaccagcag tctaccagct gagctgcagt tctagccatg 2820
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119 &lt;210&gt; SEQ ID NO: 3

120 &lt;211&gt; LENGTH: 562

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122 &lt;213&gt; ORGANISM: Homo sapiens

123 &lt;400&gt; SEQUENCE: 3

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128      Thr Ile Ala Lys Arg Glu Gly Ala Gly Asp Ala Glu Ala Asp Pro Leu
129      35          40          45
130      Glu Pro Pro Pro Pro Gln Gln Gln Leu Gly Leu Ser Leu Arg Arg Ser
131      50          55          60
132      Gly Arg Gln Pro Lys Arg Thr Glu Arg Val Glu Gln Phe Leu Thr Ile
133      65          70          75          80
134      Ala Arg Arg Arg Gly Arg Arg Ser Met Pro Val Ser Leu Glu Asp Ser
135      85          90          95
136      Gly Glu Pro Thr Ser Cys Pro Ala Thr Asp Ala Glu Thr Ala Ser Glu
137      100         105         110
138      Gly Ser Val Glu Ser Ala Ser Glu Thr Arg Ser Gly Pro Gln Ser Ala
139      115         120         125
140      Ser Thr Ala Val Lys Glu Arg Pro Ala Ser Ser Glu Lys Val Lys Gly
141      130         135         140
142      Gly Asp Asp His Asp Asp Thr Ser Asp Ser Asp Ser Asp Gly Leu Thr
143      145         150         155         160
144      Leu Lys Glu Leu Gln Asn Arg Leu Arg Arg Lys Arg Glu Gln Glu Pro

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145				165				170				175				
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147				180					185				190			
148	Arg	Glu	Glu	Gly	Pro	Ala	Glu	Thr	Val	Gly	Ser	Glu	Ala	Ser	Asp	Thr
149			195					200				205				
150	Val	Glu	Gly	Val	Leu	Pro	Ser	Lys	Gln	Glu	Pro	Glu	Asn	Asp	Gln	Gly
151		210					215				220					
152	Val	Val	Ser	Gln	Ala	Gly	Lys	Asp	Asp	Arg	Glu	Ser	Lys	Leu	Glu	Gly
153	225					230					235				240	
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155				245					250				255			
156	Pro	Lys	Pro	Glu	Cys	Glu	Gly	Tyr	Asp	Pro	Asn	Ala	Leu	Tyr	Cys	Ile
157			260						265				270			
158	Cys	Arg	Gln	Pro	His	Asn	Asn	Arg	Phe	Met	Ile	Cys	Cys	Asp	Arg	Cys
159			275					280				285				
160	Glu	Glu	Trp	Phe	His	Gly	Asp	Cys	Val	Gly	Ile	Ser	Glu	Ala	Arg	Gly
161		290					295				300					
162	Arg	Leu	Leu	Glu	Arg	Asn	Gly	Glu	Asp	Tyr	Ile	Cys	Pro	Asn	Cys	Thr
163	305					310					315				320	
164	Ile	Leu	Gln	Val	Gln	Asp	Glu	Thr	His	Ser	Glu	Thr	Ala	Asp	Gln	Gln
165				325						330				335		
166	Glu	Ala	Lys	Trp	Arg	Pro	Gly	Asp	Ala	Asp	Gly	Thr	Asp	Cys	Thr	Ser
167			340					345				350				
168	Ile	Gly	Thr	Ile	Glu	Gln	Lys	Ser	Ser	Glu	Asp	Gln	Gly	Ile	Lys	Gly
169		355					360				365					
170	Arg	Ile	Glu	Lys	Ala	Ala	Asn	Pro	Ser	Gly	Lys	Lys	Lys	Leu	Lys	Ile
171		370					375				380					
172	Phe	Gln	Pro	Val	Ile	Glu	Ala	Pro	Gly	Ala	Ser	Lys	Cys	Ile	Gly	Pro
173	385					390					395				400	
174	Gly	Cys	Cys	His	Val	Ala	Gln	Pro	Asp	Ser	Val	Tyr	Cys	Ser	Asn	Asp
175				405					410				415			
176	Cys	Ile	Leu	Lys	His	Ala	Ala	Ala	Thr	Met	Lys	Phe	Leu	Ser	Ser	Gly
177			420					425				430				
178	Lys	Glu	Gln	Lys	Pro	Lys	Pro	Lys	Glu	Lys	Met	Lys	Met	Lys	Pro	Glu
179		435					440				445					
180	Lys	Pro	Ser	Leu	Pro	Lys	Cys	Gly	Ala	Gln	Ala	Gly	Ile	Lys	Ile	Ser
181		450					455				460					
182	Ser	Val	His	Lys	Arg	Pro	Ala	Pro	Glu	Lys	Lys	Glu	Thr	Thr	Val	Lys
183	465					470					475				480	
184	Lys	Ala	Val	Val	Val	Pro	Ala	Arg	Ser	Glu	Ala	Leu	Gly	Lys	Glu	Ala
185				485					490				495			
186	Ala	Cys	Glu	Ser	Thr	Pro	Ser	Trp	Ala	Ser	Asp	His	Asn	Tyr	Asn	
187			500					505				510				
188	Ala	Val	Lys	Pro	Glu	Lys	Thr	Ala	Ala	Pro	Ser	Pro	Ser	Leu	Leu	Tyr
189		515					520				525					
190	Lys	Cys	Met	Tyr	His	Leu	Gly	Val	Gly	Leu	Leu	Asp	Pro	Ser	Arg	Ser
191		530					535				540					
192	Phe	Trp	Ile	Ala	Ile	Pro	Trp	Ala	Cys	Pro	Gly	Leu	Gly	Val	Ala	Ala
193	545					550					555				560	

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197 <211> LENGTH: 614
198 <212> TYPE: PRT
199 <213> ORGANISM: Murine spp.
200 <400> SEQUENCE: 4
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204      20              25              30
205      Thr Ile Ala Lys Arg Glu Gly Ala Gly Asp Thr Glu Ala Asp Pro Ser
206      35              40              45
207      Glu Gln Gln Pro Gln Gln His Asn Leu Ser Leu Arg Arg Ser Gly Arg
208      50              55              60
209      Gln Pro Lys Arg Thr Glu Arg Val Glu Glu Phe Leu Thr Thr Val Arg
210      65              70              75              80
211      Arg Arg Gly Lys Lys Asn Val Pro Val Ser Leu Glu Asp Ser Ser Glu
212      85              90              95
213      Pro Thr Ser Ser Thr Val Thr Asp Val Glu Thr Ala Ser Glu Gly Ser
214      100             105             110
215      Val Glu Ser Ser Ser Glu Ile Arg Ser Gly Pro Val Ser Asp Ser Leu
216      115             120             125
217      Gly Lys Glu His Pro Ala Ser Ser Glu Lys Ala Lys Gly Gly Glu Glu
218      130             135             140
219      Glu Glu Asp Thr Ser Asp Ser Asp Ser Asp Gly Leu Thr Leu Lys Glu
220      145             150             155             160
221      Leu Gln Asn Arg Leu Arg Arg Lys Arg Glu Gln Glu Pro Val Glu Arg
222      165             170             175
223      Ser Leu Arg Gly Ser Gln Asn Arg Leu Arg Lys Lys Arg Arg Glu Glu
224      180             185             190
225      Asp Ser Ala Glu Thr Gly Ser Val Gln Ile Gly Ser Ala Glu Gln Asp
226      195             200             205
227      Arg Pro Leu Cys Lys Gln Glu Pro Glu Ala Ser Gln Gly Pro Val Ser
228      210             215             220
229      Gln Ser Glu Thr Asp Asp Ile Glu Asn Gln Leu Glu Gly Lys Ala Thr
230      225             230             235             240
231      Gln Gly Asn Thr Glu Glu Asn Pro Arg Glu Ala Gly Lys Pro Lys Pro
232      245             250             255
233      Glu Cys Glu Val Tyr Asp Pro Asn Ala Leu Tyr Cys Ile Cys Arg Gln
234      260             265             270
235      Pro His Asn Asn Arg Phe Met Ile Cys Cys Asp Arg Cys Glu Glu Trp
236      275             280             285
237      Phe His Gly Asp Cys Val Gly Ile Ser Glu Ala Arg Gly Arg Leu Leu
238      290             295             300
239      Glu Arg Asn Gly Glu Asp Tyr Ile Cys Pro Asn Cys Thr Ile Leu Gln
240      305             310             315             320
241      Val Gln Asp Glu Thr Asn Gly Ser Ala Thr Asn Glu Gln Asp Ser Gly
242      325             330             335
243      Cys Arg Ser Val Gly Ala Asp Gly Thr Asp Cys Thr Ser Ile Gly Thr

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Seq#:1; Line(s) 6

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L:8 M:270 C: Current Application Number differs, Wrong Format